

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/518,174
Source: 29/10
Date Processed by STIC: 3/3/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio. (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/518,174

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/10/518,174

TIME: 12:49:08

Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\03032006\J518174.raw

5 <110> APPLICANT: Aston University
 7 <120> TITLE OF INVENTION: Methods of Producing DNA and Protein Libraries
 9 <130> FILE REFERENCE: W071488PPC
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/518,174
 C--> 12 <141> CURRENT FILING DATE: 2004-12-13
 14 <150> PRIOR APPLICATION NUMBER: GB0213816.2
 15 <151> PRIOR FILING DATE: 2002-06-14
 17 <160> NUMBER OF SEQ ID NOS: 13
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 52
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Artificial sequence
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: consensus zinc finger gene fragment
 28 <220> FEATURE:
 29 <221> NAME/KEY: misc_feature
 30 <222> LOCATION: (16)..(18)
 31 <223> OTHER INFORMATION: n=site of randomisation
 32 <220> FEATURE:
 33 <221> NAME/KEY: misc_feature
 34 <222> LOCATION: (25)..(27)
 35 <223> OTHER INFORMATION: n=site of randomisation
 37 <220> FEATURE:
 38 <221> NAME/KEY: misc_feature
 39 <222> LOCATION: (34)..(36)
 40 <223> OTHER INFORMATION: n=site of randomisation
 41 <400> SEQUENCE: 1
 W--> 42 ctgacttcga aatcannntc gctgmnnaat gttnnngtag tcgcatgctg ca 52
 43 <210> SEQ ID NO: 2
 44 <211> LENGTH: 15
 45 <212> TYPE: DNA
 46 <213> ORGANISM: Artificial sequence
 48 <220> FEATURE:
 49 <223> OTHER INFORMATION: PCR primer
 50 <400> SEQUENCE: 2
 51 gactgaagct ttagt 15
 52 <210> SEQ ID NO: 3
 53 <211> LENGTH: 16
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Artificial Sequence
 57 <220> FEATURE:
 58 <223> OTHER INFORMATION: PCR primer

pp 1-5
 Does Not Comply
 Corrected Diskette Needed

please explain N's further -
 which nucleotides
 would they represent?

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/518,174

DATE: 03/03/2006

TIME: 12:49:08

Input Set : N:\DA\pto.da.txt

Output Set : N:\CRF4\03032006\J518174.raw

59 <400> SEQUENCE: 3
60 gtcgctgggc tactac 16
62 <210> SEQ ID NO: 4
63 <211> LENGTH: 18
64 <212> TYPE: DNA
65 <213> ORGANISM: Artificial Sequence
67 <220> FEATURE:
68 <223> OTHER INFORMATION: partial complementary sequence to SEQ ID 1
69 <220> FEATURE:
70 <221> NAME/KEY: misc_feature
71 <222> LOCATION: (16)..(18)
72 <223> OTHER INFORMATION: nnn represents MAX codon (optimum codon usage for each amino acid) *Shorten line - see item 2 on Euro summary sheet*
73 in E. coli)
75 <400> SEQUENCE: 4
W--> 76 gactgaagct ttagtnnn 18
78 <210> SEQ ID NO: 5
79 <211> LENGTH: 32
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence *see item 2 on Euro summary sheet*
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Complementary sequence to SEQ ID 3 and SEQ ID 6 (partially)
85 <400> SEQUENCE: 5
86 catcagcgta cgacgtcagc gaccagatga tg 32
87 <210> SEQ ID NO: 6
88 <211> LENGTH: 42
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: consensus zinc finger gene fragment
94 <220> FEATURE:
95 <221> NAME/KEY: misc_feature
96 <222> LOCATION: (6)..(8)
97 <223> OTHER INFORMATION: n=site of randomisation
99 <220> FEATURE:
100 <221> NAME/KEY: misc_feature
101 <222> LOCATION: (15)..(17)
102 <223> OTHER INFORMATION: n=site of randomisation
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <222> LOCATION: (24)..(26)
107 <223> OTHER INFORMATION: n=site of randomisation
109 <400> SEQUENCE: 6
W--> 110 aatcannttc gctgmnnaat gttnnngtag tcgcatgctg ca 42
112 <210> SEQ ID NO: 7
113 <211> LENGTH: 15
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: PCR primer

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/518,174

DATE: 03/03/2006

TIME: 12:49:08

Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\03032006\J518174.raw

119 <400> SEQUENCE: 7
 120 atgaccatga ttacg 15
 122 <210> SEQ ID NO: 8
 123 <211> LENGTH: 30
 124 <212> TYPE: DNA
 125 <213> ORGANISM: Artificial Sequence *see item 2*
 127 <220> FEATURE:
 128 <223> OTHER INFORMATION: complementary sequence to SEQ ID 7 and SEQ ID 1 (partially)
 129 <400> SEQUENCE: 8
 130 atgaccatga ttacgctatg ccatgactga 30
 132 <210> SEQ ID NO: 9
 133 <211> LENGTH: 12
 134 <212> TYPE: DNA
 135 <213> ORGANISM: Artificial Sequence
 137 <220> FEATURE:
 139 <223> OTHER INFORMATION: partial complementary sequence to SEQ ID 1
 141 <220> FEATURE:
 142 <221> NAME/KEY: misc_feature *item 2*
 143 <222> LOCATION: (10)..(12)
 144 <223> OTHER INFORMATION: nnn represents MAX codon (optimum codon usage for each amino acid) *have over*
 145 in E. coli)
 148 <400> SEQUENCE: 9.
 W--> 149 agctttagtn nn 12
 151 <210> SEQ ID NO: 10
 152 <211> LENGTH: 15
 153 <212> TYPE: DNA
 154 <213> ORGANISM: Artificial Sequence
 156 <220> FEATURE:
 157 <223> OTHER INFORMATION: PCR primer
 158 <400> SEQUENCE: 10
 159 acttgagact gaagc 15
 161 <210> SEQ ID NO: 11
 162 <211> LENGTH: 15
 163 <212> TYPE: DNA
 164 <213> ORGANISM: Artificial Sequence
 166 <220> FEATURE:
 167 <223> OTHER INFORMATION: PCR primer
 168 <400> SEQUENCE: 11
 169 gcatgctaga ctgcc 15
 171 <210> SEQ ID NO: 12
 172 <211> LENGTH: 21
 173 <212> TYPE: DNA
 174 <213> ORGANISM: Artificial Sequence
 176 <220> FEATURE:
 177 <223> OTHER INFORMATION: complementary sequence to SEQ ID 11 and SEQ ID 13 (partially) *have over*
 178 <400> SEQUENCE: 12
 179 catcagcgta cgatctgacg c 21
 182 <210> SEQ ID NO: 13
 183 <211> LENGTH: 39

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/518,174

DATE: 03/03/2006

TIME: 12:49:08

Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\03032006\J518174.raw

184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: consensus zinc finger gene fragment
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: (13)..(15)
192 <223> OTHER INFORMATION: n=site of randomisation
194 <220> FEATURE:
195 <221> NAME/KEY: misc_feature
196 <222> LOCATION: (22)..(24)
197 <223> OTHER INFORMATION: n=site of randomisation
199 <220> FEATURE:
200 <221> NAME/KEY: misc_feature
201 <222> LOCATION: (31)..(34)
202 <223> OTHER INFORMATION: n=site of randomisation
204 <400> SEQUENCE: 13

W--> 205 acttcgaaat canntcgct gnnnaatggt nngtagtc

W--> 206 25567341.1 - 5

*delete**(33) 'g' is at location 4*

39

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/518,174

DATE: 03/03/2006
TIME: 12:49:09

Input Set : N:\DA\pto.da.txt
Output Set: N:\CRF4\03032006\J518174.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 16,17,18,25,26,27,34,35,36
Seq#:4; N Pos. 16,17,18
Seq#:6; N Pos. 6,7,8,15,16,17,24,25,26
Seq#:9; N Pos. 10,11,12
Seq#:13; N Pos. 13,14,15,22,23,24,31,32,33

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/518,174

DATE: 03/03/2006

TIME: 12:49:09

Input Set : N:\DA\pto.da.txt

Output Set: N:\CRF4\03032006\J518174.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:206 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4